

**Exhibit A**

**Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/714,882**

1.(Amended) An isolated nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1.

2.(Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:2.

3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.

4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.

5 An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.

6. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.

7.(New) An expression vector comprising a nucleic acid sequence of Claim 2.

8.(New) A cell comprising the expression vector of Claim 7.

**Exhibit B**

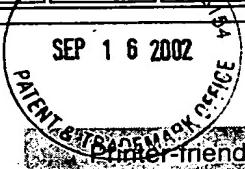
**Marked-up Version of The Pending Claims in U.S. Patent Application Ser. No. 09/714,882**

1. An isolated nucleic acid molecule comprising [at least 24 contiguous bases of] the nucleotide sequence [first disclosed in the NHP sequence described] shown in SEQ ID NO:1.
  
2. An isolated nucleic acid molecule comprising a nucleotide sequence that[:  
    (a) ]encodes the amino acid sequence shown in SEQ ID NO:2[; and  
    (b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof].
  
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4.
  
4. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:6.
  
- 5 An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:8.
  
6. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:10.
  
- 7.(New) An expression vector comprising a nucleic acid sequence of Claim 2.
  
- 8.(New) A cell comprising the expression vector of Claim 7.

<a href="#">ExPASy Home page</a>	<a href="#">Site Map</a>	<a href="#">Search ExPASy</a>	<a href="#">Contact us</a>	<a href="#">SWISS-PROT</a>
Hosted by NCSC US	Mirror sites:	<a href="#">Canada</a> <a href="#">China</a> <a href="#">Korea</a> <a href="#">Switzerland</a> <a href="#">Taiwan</a>		

# NiceProt View of TrEMBL: Q9UGD3

[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features]  
[\[Sequence\]](#) [\[Tools\]](#)



[Quick BlastP search](#)

## General information about the entry

RECEIVED

Entry name	Q9UGD3	SEP 18 2002
Primary accession number	Q9UGD3	
Secondary accession numbers	None	TECH CENTER 1600/2900
Entered in TrEMBL in	Release 13, May 2000	
Sequence was last modified in	Release 17, June 2001	
Annotations were last modified in	Release 22, October 2002	
<b>Name and origin of the protein</b>		
Protein name	DJ842G6.2 [Fragment]	
Synonym	Novel protein imilar to SEL1L (Sel-1 (Suppressor of lin-12, C.elegans)-like)	
Gene name	DJ842G6.2	
From	<u>Homo sapiens</u> ( <u>Human</u> ) [TaxID: <u>9606</u> ]	
Taxonomy	<u>Eukaryota</u> ; <u>Metazoa</u> ; <u>Chordata</u> ; <u>Craniata</u> ; <u>Vertebrata</u> ; <u>Euteleostomi</u> ; <u>Mammalia</u> ; <u>Eutheria</u> ; <u>Primates</u> ; <u>Catarrhini</u> ; <u>Hominidae</u> ; <u>Homo</u> .	

## References

- [1] SEQUENCE FROM NUCLEIC ACID.  
Barlow K.,  
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

## Comments

None

## Cross-references

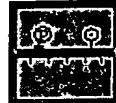
EMBL	AL109657; CAB65792.2; -.[ <a href="#">EMBL</a> / <a href="#">GenBank</a> / <a href="#">DDBJ</a> ] [ <a href="#">CoDingSequence</a> ]
Genew	<a href="#">HGNC:15897</a> ; <a href="#">C20orf50</a> .
Ensembl	Q9UGD3; <u>Homo sapiens</u> . [ <a href="#">Entry</a> / <a href="#">Contig view</a> ]
ProtoMap	<a href="#">Q9UGD3</a> .
PRESAGE	<a href="#">Q9UGD3</a> .
ModBase	<a href="#">Q9UGD3</a> .
SWISS-2DPAGE	<a href="#">GET REGION ON 2D PAGE</a> .

## Keywords

None

## Features

Key From To Length Description  
NON\_TER 1 1



[Feature table viewer](#)

### Sequence information

Length: 505 AA [This is the length of the partial sequence]  
Molecular weight: 57003 Da [This is the MW of the partial sequence]

CRC64: 536D4361FA826E35 [This is a checksum on the sequence]

10	20	30	40	50	60
ALGFLSSYGI	GMEYDQAKAL	IYYTFSAGG	NMMSQMILGY	RYLSGINVLQ	NCEVALSYYK
70	80	90	100	110	120
KVADYIADTF	EKSEGVVPVEK	VRLTERPENL	SSNSEILDWD	IYQYYKFLAE	RGDVQIQVSL
130	140	150	160	170	180
GQLHLIGRKG	LDQDYYKALH	YFLKAAKAGS	ANAMAFIGKM	YLEGNAAVPQ	NNATAFKYFS
190	200	210	220	230	240
MAASKGNAIG	LHGLGLLYFH	GKGVPPLNYAE	ALKYFQKAAE	KGWPDAQFQL	GFMYYSGSGI
250	260	270	280	290	300
WKDYKLAFKY	FYLASQSGQP	LAIYYLAKMY	ATGTGVRSC	RTAVELYKGV	CELGHWAEKF
310	320	330	340	350	360
LTAYFAYKDG	DIDSSLVQYA	LLAEMGYEVA	QSNSAFILES	KKANILEKEK	MYPMALLLWN
370	380	390	400	410	420
RAAIQGNAFA	RVKIGDYHYY	GYGTTKDYQT	AATHYSIAAN	KYHNAQAMFN	LAYMYEHGLG
430	440	450	460	470	480
ITKDIHLARR	LYDMAAQQTSP	DAHIPVLFAV	MKLETTHLLR	DILFFNFTTR	WNWLKLDNTI
490	500				
GPHWDLFVIG	LIVPGLLLLL	RNHHG			

**RECEIVED**

SEP 18 2002

TECH CENTER 1600/2900

[View entry in original TrEMBL format](#)

[View entry in raw text format \(no links\)](#)

[Request for annotation of this TrEMBL entry](#)



Direct BLAST submission at  
[EMBnet-CH/SIB \(Switzerland\)](#)



Direct BLAST submission at [NCBI \(Bethesda, USA\)](#)

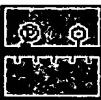
Sequence analysis tools: [ProtParam](#), [ProtScale](#),



[ScanProsite](#), [MotifScan](#)

Tools

[Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#),  
[Dotlet \(Java\)](#)



[Feature table viewer \(Java\)](#)



[Search the SWISS-MODEL Repository](#)

[ExPASy Home page](#)

[Site Map](#)

[Search ExPASy](#)

[Contact us](#)

[SWISS-PROT](#)

Hosted by NCSC US

Mirror sites:

[Canada](#)

[China](#)

[Korea](#)

[Switzerland](#)

[Taiwan](#)

## EXHIBIT "D"

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
/tmp/fastaCAA_Xa4Ot: 689 aa
>FIRST_SEQUENCE
vs /tmp/fastaDAAaYa4Ot library
searching /tmp/fastaDAAaYa4Ot library
```

505 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 38, opt: 26, gap-pen: -12/ -2, width: 16  
Scan time: 0.033

The best scores are:  
tr|Q9UGD3 DJ842G6.2 (Novel protein imilar to SEL1 ( 505) 3344 opt

```
>>tr|Q9UGD3 DJ842G6.2 (Novel protein imilar to SEL1L (Se (505 aa)
initn: 3342 initl: 3071 opt: 3344
Smith-Waterman score: 3344; 99.802% identity in 506 aa overlap (184-689:1-505)
```

160	170	180	190	200	210
FIRST_ LFGNFGVQNITAAIQLYESLAKEGSCKAQNALGFLSSYGIGMEYDQAKALIYYT					

tr Q9U			ALGFLSSYGIGMEYDQAKALIYYT		
				20	30

220	230	240	250	260	270
FIRST_ NMMSQMILGYRYLSGINVLQNCEVALSYKKVADYIADTFEKSEGVPVEKVR					

tr Q9U NMMSQMILGYRYLSGINVLQNCEVALSYKKVADYIADTFEKSEGVPVEKVR					
	40	50	60	70	80
					90

280	290	300	310	320	330
FIRST_ SSNSEILDWDIYQYYKFLAERGVQIQVSLGQLHLIGRKGLDQDYYKALHYFL					

tr Q9U SSNSEILDWDIYQYYKFLAERGVQIQVSLGQLHLIGRKGLDQDYYKALHYFL					
	100	110	120	130	140
					150

340	350	360	370	380	390
FIRST_ ANAMAFIGKMYLEGNAAVPQNNATAFKYFSMAASKGNAIGLHGLGLLYFHGKVPL					

tr Q9U ANAMAFIGKMYLEGNAAVPQNNATAFKYFSMAASKGNAIGLHGLGLLYFHGKVPL					
	160	170	180	190	200
					210

400	410	420	430	440	450
FIRST_ ALKYFQKAAEKGPDAQFQLGFMYSGSGIWKDYKLAFKYFYLASQSGQPLAIYYL					

tr Q9U ALKYFQKAAEKGPDAQFQLGFMYSGSGIWKDYKLAFKYFYLASQSGQPLAIYYL					
	220	230	240	250	260
					270

460	470	480	490	500	510
FIRST_ ATGTGVVRSCRTAVELYKGVC	ELGHWA	EKF	TAYFAY	KDG	DIDSSLV

tr Q9U ATGTGVVRSCRTAVELYKGVC	ELGHWA	EKF	TAYFAY	KDG	DIDSSLV
	280	290	300	310	320
					330

520	530	540	550	560	570
FIRST_ QSNSAFILESKKANILEKEK	MYP	MA	LLWNRAAI	QGN	FA

tr|Q9U QNSAFILESKKANILEKEKMYPMALLWNRAAIQGNAFARVKIGDYHYYGYGTKKDYQT  
340 350 360 370 380 390  
580 590 600 610 620 630  
FIRST\_ AATHYSIAANKYHNAQAMFNLAYMYEHGLGITKDIHLARRLYDMAAQTS PDAHIPVLF  
tr|Q9U AATHYSIAANKYHNAQAMFNLAYMYEHGLGITKDIHLARRLYDMAAQTS PDAHIPVLF  
400 410 420 430 440 450  
640 650 660 670 680  
FIRST\_ MKLETTHLLRDILFFNQFTTRWNWLKDNTIGPHWDLFVIGLIVPGLILLLRNH  
tr|Q9U MKLETTHLLRDILFFN-QFTTRWNWLKDNTIGPHWDLFVIGLIVPGLILLLRNH  
460 470 480 490 500

689 residues in 1 query sequences  
505 residues in 1 library sequences  
Scomplib [version 3.3t05 March 30, 2000]  
start: Fri Sep 6 11:53:40 2002 done: Fri Sep 6 11:53:40 2002  
Scan time: 0.033 Display time: 0.434

Function used was FASTA